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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

hypothetical protein pH0368 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 08-Sep-2000
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 08-Sep-2000
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 08-Sep-2000
C;Accession: E71144
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogh
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogh
DNA Res. 5, 55-76, 1998
A,;Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A,;Reference number: A71000; MUID:98344137 RESULT E71144 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-364 <KAW> A;Cross-references: GB:AP000002; NID:g3236129; PIDN:BAA29442.1; PID:d1030385; PID:g32 A;Experimental source: strain OT3 A;Note: this accession replaces an interim accession for a sequence replaced by GenBa A;Gene: PH0368 C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0368 C; Genetics: A; Accession: E71144 Query Match Best Local Similarity Matches 275; Conserv 79.6%; Score 1494; DB 2; Pred. No. 2.7e-105; Length 364;

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		361 NGE 363	Qy
	360	301 DKSLRIWKEDEGNARLNMLTYCMDGEFAFLAENSDARGWEPLPERRLDAFKAIYKYWRNE 360	Дb
	E 360	301 DKSLRIWREDEGNARLNWLSYNWRGELALLAENSDARGWEPLPERRLDAFRAIYNDWRGE	Qy
	300	241 EILLYGTDIEFLGYRSIAGHKIAISGLMEVLNELGGELCLPRDIRHNGRRLYLRTSSWAP	Дb
	300	241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP	Qy
	240	181 LRELKKAINLTFGGKVTLEAVKDIEAIPVWVSINIAIMLGAGREPLMSPKRVANWIKGKD	Дb
	240	181 LRELRKAIKLYFEGKVTLKAVKDIEAVPYWVAVNTAVNLGIGRLPLMNPKKVASWIEDKD	Qy
	180	121 DPIIPAILRDNEYEYLFADGEAMLFSNHLNSAIKSIKPLYPYLIKAQRGBGFVYLNYLLG	Дb
	180	121 DPIIPAILKDNGYEYLFADGEAMLFSAHLNSAIKPIKPLYPHLIKAQREKRFRYISYLLG	Qy
	120	61 LIKEGIESELIEILGTSYTHAILPLLTLSRIEAQIKRDREIKEEIFEVSPGGFWLPELAY	Db
	120	61 LYKGGIASDLIEIIGTSYTHAILPLLPLSRVEAQVQRDREVKEELFELSPKGFWLPELAY	Qy
4	1 60	1 MRALIFHGNLQYAEIPKHEISKVIEKSYFPTISELIKREIPFGLNITGYSLQFLPQELIH	рь
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A;Molecule type: DNA
A;Residues: 1-529 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74149.1; PID:g17131542; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr450
A;Gene: alr450
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1386
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R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
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                                     6803)
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A;Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18743.1; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1386
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A; Residues: 1-529 < KAN>
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A;Accession: S76831
A;Status: preliminary
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C;Accession: S76831
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
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423 WIYPHLHKAAERMIELSHREAVDELEEK----ALNQAARELLLAQSSDWA
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Pred. No. 0.00017;
7; Mismatches 140;
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probable alpha-amylase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Ju1-2000 C; Accession: G71241

DNA Res. R; Kawarabayasi, Y.; Sawada, M.; Ohfuku, Y.; Funahashi, 5, 55-76, 1998 H K Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, of a hyper-thermophili z : : ; Se Ogu

A;Title: Complete sequence and gene organization of the genome A;Reference number: A71000; MUID:98344137 A;Accession: G71241

not shown

GenBa

A;Residues: A; Molecule type: DNA A; Status: preliminary; nucleic acid sequence not shown; translation 1-633 <KAW>

A; Experimental source: strain OT3 A; Note: this accession replaces an interim accession for a sequence replaced by A;Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29262.1; PID:g3256579

C; Genetics:

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                                                                        INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                               REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPHONE: 619-678-5070
                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
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APPLICATION NUMBER:
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APPLICANT: Reid, John
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                                             TYPE:
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ZIP: 92037
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STATE: CA
                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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4225 Executive Square, Suite 1400
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GENERAL INFORMATION:
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Best Local (
                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                  ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STATE: C
COUNTRY:
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                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                             TELEFAX: 619-68-5099
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: CA
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Pred. No. 3.4e-152;
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